

w66989 ; TOIG of: w66989 check: 1388 from: 1 to: 366

LOCUS W66989 366 bp mRNA linear EST 14-JUN-1996

DEFINITION me30a03_r1 Soares mouse embryo NbME13.5 14-5 Mus musculus cDNA

clone IMAGE:388972 5' similar to WP:F55G12.9 CE00978 ; mRNA sequence

ACCESSION W66989.1 GI:1375916

VERSION EST.

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

MG:240894

Seq primer: mob.REGA+ET

High quality sequence stop: 354.

FEATURES

Source

Location/Qualifiers

1..366

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref=taxon:10090"

/clone="IMAGE:388972"

/sex="unknow"

/tissue_type="embryo"

/dev_stage="13.5-1.5dpc total fetus"

/lab_host="DH10B"

/clone_id="Soares mouse embryo NbME13.5 14-5"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with $\tilde{5}$ Not I - oligo(dT) primer [5', TGTACCAACTGAGTGGAGGCGGAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minou Ko, Wayne State Univ., from 2); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaido. "

ORIGIN

w66989 Length: 366 June 23, 2005 12:30 Type: N Check: 1388 ..

Query Match 78.9% Score 257.9; DB 1; Length 366;

Best Local Similarity 90.0%; Pred. No. 0.98; Mismatches 0; Indels 1; Gaps 1;

Matches 287; Conservative 0; Gaps 1;

Qy 10 GCGATGGATGGATAACCGGAGGGCACCAACGGGGGGCAAGAGCCCTTCGA 69

Db 31 GGGATGGATGGATAACCCCAAGGGCACCAACGGGGGGCAAGAGCCCTTCGA 90

Qy 70 GTGAAAAGTGGAAATGAGTAGCCCTCTGGCTGGATATTG-TGGTGTAACTGTG 128

Db 91 GTTAAAGTGGAAATGGAGTGGCCCTCTGGCTGGATATTGCTGTGATAACTGTG 150

Qy 129 CATCTGGAGAACCAATTATGGATTTGATAGAATGTCAGCTTCAAGCTAACCGGGTCGC 188

Db 151 CATCTGGAGAACCAATTATGGATTTGATAGTCAGCTTCAAGCTAACCGGGTCGC 210

Qy 189 TACTCTGAGAGTGTACTGCGCATGGGACTCTGTAACCATGCTTCACTTCAGT 248

Db 211 TACTCTGAGAGTGTACTGCGCATGGGACTCTGTAACCATGCTTCACTTCAGT 270

Qy 249 CATCTCTGGCTCAAACGAGAGTGTCAATTGGACAAAGAGACTGGGATT 308

Db 271 CATCTCTGGCTCAAACGAGAGTGTCAATTGGACAAAGAGACTGGGAGTT 330

RESULTS 3

aa260899

; TOIG of: aa260899 check: 515 from: 1 to: 479

LOCUS AA260899 479 bp mRNA linear EST 18-MAR-1997

DEFINITION Va01h09.rl Soares mouse lymph node NbMLN Mus musculus cDNA Clone IMAGE:721697 5, similar to WP:2K287.5 CE06614 ; mRNA sequence.

ACCESSION AA260899

VERSION AA260899.1 GI:1897377

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Mammalia: Eutheria; Rodentia; Vertebrata; Butteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 479)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

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MG:447193

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 400.

Location/Qualifiers

1..479

Source

/mol_type="mRNA"

/strain="C57BL/6J"

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/clone="IMAGE:388972"

/sex="male"

/tissue_type="lymph node"

/dev_stage="4 weeks"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:721697"

/sex="male"

/tissue_type="lymph node"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Soares mouse lymph node NbMLN"

/note="Organ: lymph node; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with $\tilde{5}$ Not I - oligo(dT) primer [5', TGTACCAACTGAGTGGAGGCGGAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I - oligo(dT) primer and Eco RI sites of the modified pT7T3 vector. RNA


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Location/Qualifiers
 1. .403
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="GDB:3778670"
  /db_xref="Taxon:9606"
  /clone="IMAGE:2133366"
  /sex="male"
  /dev_stage="20 week-post conception fetus"
  /lab_host="DH10B (ampicillin resistant)"
  /clone_lib="Soares fetal liver spleen 1NFLS"
  /note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGAAGTAAATAAGCTCTTCTTCTTCTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
  /ORIGIN
  H71993 Length: 403 June 23, 2005 12:30 Type: N Check: 7893 ...
  n1993

  Query Match 5.3%; Score 17.4; DB 1; Length 403;
  Best Local Similarity 49.5%; Pred. No. 5.3;
  Matches 45; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
  w66989 Length: 366 June 23, 2005 12:30 Type: N Check: 1388 ...
  w66989

  Query Match 4.2%; Score 13.8; DB 1; Length 366;
  Best Local Similarity 58.5%; Pred. No. 5.9;
  Matches 24; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
  Qy 205 ACTGTCGATGGGGTGTGTAACCATGCTTTCACTTCCA 245
  Db 126 ACGCACCGAGGGCCACCTGATTCACCTTTAACTCAA 86

  Search completed: June 23, 2005, 12:35:20
  Job time : 1 secs

  RESULT 6
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  ; TOIG of: w66989 check: 1388 from: 1 to: 366

  LOCUS W66989 366 bp mRNA linear EST 14-JUN-1996
  DEFINITION me30a03_r1 Soares mouse embryo NAME:13.5 14.5 Mus musculus cDNA
  ; Sequence.
  W66989
  ; ACCESSION W66989.1 GI:1375916
  ; VERSION
  ; KEYWORDS EST.
  ; SOURCE Mus musculus (house mouse)
  ; ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  ; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  ; REFERENCE 1 (bases 1 to 366)
  ; AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schenlemburg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
  ; TITLE The WashU HHMI Mouse EST Project
  ; JOURNAL Unpublished (1996)
  ; COMMENT Contact: Marra M/Mouse EST Project
  ; WASHU-HHMI Mouse EST Project
  ; Washington University School of Medicine
  ; 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  ; Tel: 314 286 1800
  ; Fax: 314 286 1810
  ; Email: mouseest@washburn.wustl.edu
  ; This clone is available royalty-free through LBNL; contact the
  ; IMAGE Consortium (info@image.llnl.gov) for further information.
  ; MGI:240804
  ; Seq. p: Quality sequence stop: 354
  ; Seq. p: mod: RGA+ET
  ; High quality sequence stop: 354

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
 Run on: June 23, 2005, 12:36:48 ; Search time 0.001 Seconds
 (without alignments) 269.568 Million cell updates/sec

Title: US-09-541-462B-2
 Perfect score: 616
 Sequence: 1 MAAMDDVTPSGCTNSGAGKK. KTRQVCPLDNREMEFQKYGH 108

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delett 7.0

Searched: 3 seqs, 1248 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Command line parameters:
 -MDBL=Frame+52n model -DBV=soft -Q=US09541462B..ped -DB=gb seq -SUFFIX=pto
 -OUT=aa..res -MINMATCH=0.1 -LOOPCL=0 -UNITS=bits -START=1 -END=-1
 -MATRIX=BLOSUM62 -TRANS:human40.cdt -LIST=45 -DOALIGN=300 -THR SCOREB=pct
 -THR MAX=100 -THR MIN=0 -ALIGN=5 -MODE=LOCAL -OUTPMT=pto -NORM=ext
 -HEAFSIZE=500 -MINLEN=200000000 -NCPU=6 -NO_XLIPXY -NEG_SCORES=0
 -LONGLINK -THREADS=1 -XGAPOP=10 -XGAPEXT=7 -YGAPOP=6 -FGAPEXT=7 -YGAPOP=10
 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : gb.seq *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	87.5	366	1 w66989	TOIG of: w66989
2	520.5	86.0	403	1 h71993	TOIG of: h71993
c 4	44.5	7.2	479	1 aa260889	TOIG of: aa260889
c 5	42	6.8	366	1 w66989	TOIG of: w66989
c 6	39	6.3	403	1 h71993	TOIG of: h71993

ALIGNMENTS

RESULT 1

TOIG of:	w66989	check:	w66989	from:	1	to:	366
LOCUS	W66989						
DEFINITION	me30a03.r1	Soares mouse embryo	366 bp	mRNA	linear	EST 14-JUN-1996	
						Clone IMAGE3.388972 5'	similar to WP:F35G12.9 CSD0978 ; mRNA
ACCESSION	W66989						Sequence.
VERSION	W66989.1						GI:1375916

US-09-541-462B-2 (1-108) x w66989 (1-366)

QY 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysArgPheGluVal 24
 TOIG of: w66989

DB 34 ATGGATGTGATACCCCAAGGGCACCAACGGGGCGCAAGAGCGCTTGAGTT 93

QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaPhe-ValValAspAsnCysAlaI 44
 TOIG of: w66989

DB 94 ARAAATGGATGTGAGCTCGCTCGTGTGAGATTGTGTGATACTGTGCT 153

QY 44 eCysArgAsnHisIleMetAspLeuCysGlnAlaArgGlnAlaSerAlaL 64

h71993 Length: 403 June 23, 2005 12:30 Type: N Check: 7893 ..

Alignment Scores:
Pred. No.: 5.25 Length: 403
Score: 39.00 Matches: 11
Percent Similarity: 41.38% Conservative: 1
Best Local Similarity: 37.93% Mismatches: 9
Query Match: 6.33% Indels: 8
DB: 1 Gaps: 1

US-09-541-462B-2 (1-108) x h71993 (1-403)

Qy 74 ValCysAsnHis-----AlaPheHisPheHisCysIleSer 85
Db 125 GTTATCAACACAATAATCCCNAGCCAGAGGGCTACTGCATTCACCTTCACTTCAAAG 66

Qy 86 ArgTrpIleLysThrArgGlnValCys 94
Db 65 CGCTTCCTGCNCAGCCGCTGTTGGTGC 39

Search completed: June 23, 2005, 12:36:48
Job time : 0.001 secs

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